

JUL 06 1998

Attorney Docket No. E1047/20006

SEQUENCE LISTING

PATENT & TRADEMARK OFFICE

GENERAL INFORMATION:

- (i) APPLICANTS: Yuan Min Wu and Eileen Xiao-Feng Nie
(ii) TITLE OF THE INVENTION: SOLUTION HYBRIDIZATION OF
NUCLEIC ACIDS WITH ANTISENSE
PROBES HAVING MODIFIED BACKBONES

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Caesar, Rivise, Bernstein, Cohen & Pokotilow, Ltd.
(B) STREET: 12th Floor, 7 Penn Center, 1635 Market Street
(C) CITY: Philadelphia
(D) STATE: Pennsylvania
(E) COUNTRY: U.S.A.
(F) ZIP: 19103-2212

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Tener, David M.
(B) REGISTRATION NUMBER: 37,054
(C) REFERENCE/DOCKET NUMBER: E1047/20006

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 215-567-2010
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30 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 bases
(B) TYPE: nucleotide
(C) STRANDEDNESS: double-stranded
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTTCGAGATG TTCCGAGAGC TGAATGAGGC CTTGGAACTC 40

(2) INFORMATION FOR SEQ ID NO:2:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 bases
(B) TYPE: nucleotide
(C) STRANDEDNESS: double-stranded

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTTCGAGATG TTCCGAGAGC AGAATGAGGC CTTGGAACTC 40

(2) INFORMATION FOR SEQ ID NO:3:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTCGAGATG TTCCGAGAGG AGAATGAGGC CTTGGAACTC 40

(2) INFORMATION FOR SEQ ID NO:4:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTTCGAGATG TTCCGAGAGT ACAATGAGGC CTTGGAACTC 40

20 (2) INFORMATION FOR SEQ ID NO:5:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACACCAGCT CCTCTCCCCA GCCAAAGAAG AAACCCTGG 40

30 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AACACCAGCT CCTCTCCCCA GCCAAAGAAG AAACCCTGG ATGGAGAATA TTTCACCCCTT 60

CAGATCCGTG GGC GTGAGCG CTT CGAGATG TTCCGAGAGC TGAATGAGGC CTTGGAACTC 120

AAGGATGCC AGGCTGGAA GGAGCCAGGG 150

(2) INFORMATION FOR SEQ ID NO:7:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

10 AACACCAGCT CCTCTCCCCA GCCAAAGAAG AAACC ACTGG ATGGAGAATA TTTCACCCCTT 60

CAGATCCGTG GGC GTGAGCG CTT CGAGATG TTCCGAGAGC AGAATGAGGC CTTGGAACTC 120

AAGGATGCC AGGCTGGAA GGAGCCAGGG 150

(2) INFORMATION FOR SEQ ID NO:8:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AACACCAGCT CCTCTCCCCA GCCAAAGAAG AAACC ACTGG ATGGAGAATA TTTCACCCCTT 60

CAGATCCGTG GGC GTGAGCG CTT CGAGATG TTCCGAGAGA AGAATGAGGC CTTGGAACTC 120

AAGGATGCC AGGCTGGAA GGAGCCAGGG 150

(2) INFORMATION FOR SEQ ID NO:9:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double-stranded
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCCAACTGGC CAAGACCTGC CCTGTGCAGC TGTGGTTGA TTCCACACCC CCGCCCGGCA 60

CCCGCGTCCG CGCCATGGCC ATCTACAAGC AGTCACAGCA CATGACGGAG GTTGTGAGGC 120

(2) INFORMATION FOR SEQ ID NO:10:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases

- (B) TYPE: nucleotide with four methylphosphonate substitutions along its backbone
- (C) STRANDEDNESS: single-stranded
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCTCATTCAAG CTCTCGGA 18

(2) INFORMATION FOR SEQ ID NO:11:

- 10 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: nucleotide with nine methylphosphonate substitutions along its backbone
 - (C) STRANDEDNESS: single-stranded
 - (D) TOPOLOGY: linear

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Cont 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTCATTCAAG CTCTCGGA 18

(2) INFORMATION FOR SEQ ID NO:12:

- 20 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 bases
 - (B) TYPE: nucleotide with 15 methylphosphonate substitutions along its backbone
 - (C) STRANDEDNESS: single-stranded
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCATTCAAGC TCTCG 15
